

Glycophorin B is the erythrocyte receptor of *Plasmodium falciparum* erythrocyte-binding ligand, EBL-1

D. C. Ghislaine Mayer^{a,1}, Joann Cofie^a, Lubin Jiang^b, Daniel L. Hartl^c, Erin Tracy^a, Juraj Kabat^d, Laurence H. Mendoza^a, and Louis H. Miller^{a,1}

^aDepartment of Biology, Virginia Commonwealth University, 1000 West Cary Street, Room 126, Richmond, VA 23284-2012; ^bLaboratory of Malaria Vector Research, 12735 Twinbrook Parkway, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Rockville, MD 20852; ^cBiological Imaging Section, Research Technologies Branch, National Institute of Allergy and Infectious Diseases, National Institutes of Health, 4 Center Drive, MSC 0485, Bethesda, MD 20892; and ^dDepartment of Organismic and Evolutionary Biology, Harvard University, 16 Divinity Avenue, Cambridge, MA 02138

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In the war against *Plasmodium*, humans have evolved to eliminate or modify proteins on the erythrocyte surface that serve as receptors for parasite invasion, such as the Duffy blood group, a receptor for *Plasmodium vivax*, and the Gerbich-negative modification of glycophorin C for *Plasmodium falciparum*. In turn, the parasite counters with expansion and diversification of ligand families. The high degree of polymorphism in glycophorin B found in malaria-endemic regions suggests that it also may be a receptor for *Plasmodium*, but, to date, none has been identified. We provide evidence from erythrocyte-binding that glycophorin B is a receptor for the *P. falciparum* protein EBL-1, a member of the Duffy-binding-like erythrocyte-binding protein (DBL-EBP) receptor family. The erythrocyte-binding domain, region 2 of EBL-1, expressed on CHO-K1 cells, bound glycophorin B⁺ but not glycophorin B-null erythrocytes. In addition, glycophorin B⁺ but not glycophorin B-null erythrocytes adsorbed native EBL-1 from the *P. falciparum* culture supernatants. Interestingly, the Efe pygmies of the Ituri forest in the Democratic Republic of the Congo have the highest gene frequency of glycophorin B-null in the world, raising the possibility that the DBL-EBP family may have expanded in response to the high frequency of glycophorin B-null in the population.

Duffy-binding-like erythrocyte-binding protein | invasion | malaria | red blood cells

The asexual erythrocytic phase of the life cycle of *Plasmodium falciparum* produces all of the clinical symptoms, disease, and pathology associated with malaria. During this phase, merozoites released from schizont-infected erythrocytes invade uninfected erythrocytes. Invasion depends on distinct molecular interactions between ligands on the merozoite, the invasive form of the parasite, and host receptors on the erythrocyte membrane. To avoid infection, humans have evolved to eliminate or modify erythrocyte surface proteins that serve as receptors for parasite invasion. Perhaps one of the best examples of this evolutionary process is the loss of the Duffy blood group in Africa. *Plasmodium vivax* depends on two ligands for erythrocyte invasion: the Duffy-binding protein (DBP) that binds the Duffy blood group antigen (1, 2) and the reticulocyte homology protein that binds to an unknown receptor on reticulocytes (3). The Duffy blood group-null went almost to fixation in West Africa and is being selected in Papua New Guinea as a result of the inability of *P. vivax* to invade Duffy-negative erythrocytes (4).

Unlike *P. vivax*, *P. falciparum* has highly redundant, alternate invasion pathways that use several different receptor families. For example, *P. vivax* has only one gene, DBP, in the Duffy-binding-like erythrocyte-binding protein (DBL-EBP) family, whereas *P. falciparum* has four DBL-EBP genes: erythrocyte-binding antigen 175 (EBA-175), erythrocyte-binding antigen 140 (BAEBL/EBA-140), erythrocyte-binding antigen 181 (JESEBL/EBA-181), and erythrocyte-binding ligand-1 (EBL-1) (5–10).

Consequently, no erythrocyte has been identified that is refractory to *P. falciparum* invasion. The erythrocyte-binding domains for *P. vivax* DBL-EBP and for three of the *P. falciparum* DBL-EBPs reside in the N-terminal cysteine-rich region, region 2 (8, 11, 12). In *P. falciparum*, the region 2 domain is duplicated; both domains are required for optimum binding to erythrocytes. The erythrocyte receptors for the *P. falciparum* DBL-EBPs include glycophorin A for EBA-175 and glycophorin C for one of the BAEBL/EBA-140 proteins (6, 12). The receptor for JESEBL/EBA-181 is not known. No *P. falciparum* ligand has been found to bind glycophorin B, even though glycophorin B is highly polymorphic, suggesting that it is under a strong selective pressure. The polymorphisms are especially high in Africans and in African-Americans where multiple mutations exist, including the S-s-U-blood group (glycophorin B-null) that has a gene frequency of 59% in the Ituri forest pygmies (13, 14).

Here, we provide evidence that the fourth DBL-EBP family member, EBL-1, binds to glycophorin B. Region 2 of EBL-1 expressed on CHO-K1 cells bound to normal erythrocytes but failed to bind S-s-U- erythrocytes that lack glycophorin B. Furthermore, EBL-1 immunoprecipitated from *P. falciparum* culture supernatant bound to normal erythrocytes but not to S-s-U- erythrocytes. EBL-1 also fails to bind chymotrypsin- and neuraminidase-treated erythrocytes, consistent with the erythrocyte receptor being glycophorin B, a protein that is sensitive to neuraminidase and chymotrypsin. Thus, these studies identify glycophorin B as the erythrocyte receptor of EBL-1.

Results

Localization of EBL-1. The spatial and temporal expression of EBL-1 has not been reported. To verify that the location of EBL-1 is similar to that of other members of the DBL-EBP family, we localized EBL-1 by fluorescent confocal microscopy. Antibodies specific for region 2 of EBL-1 of the *P. falciparum* clone Dd2/Nm colocalized with RAP1, a rhoptry marker, and BAEBL, a microneme marker (Fig. 1). Despite the apparent complete colocalization of EBL-1-specific antibodies with RAP1 and partial colocalization with BAEBL antibodies, the

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The authors declare no conflict of interest.

Data deposition: The sequences reported in this paper have been deposited in the GenBank database (accession no. FJ392548).

¹To whom correspondence may be addressed. E-mail: gmayer@vcu.edu or lmiller@niaid.nih.gov.

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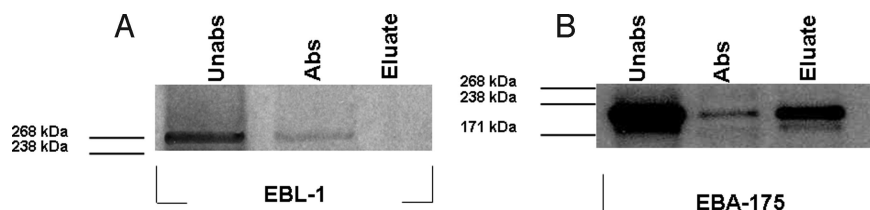


Fig. 4. EBL-1 does not bind to S-s-U- erythrocytes that lack glycophorin B. Proteins in culture supernatant were adsorbed to S-s-U- erythrocytes. The supernatant and the eluate were immunoprecipitated with antibodies to EBL-1 (A) or to EBA-175 (B).

We further investigated the binding specificity of region 2 of EBL-1 by expressing it as a fusion protein in the pRE4 vector, as described in ref. 15. As a control, we expressed the extracellular region of EBL-1 near the transmembrane sequence. For all transfected constructs, positive surface expression was confirmed by immunofluorescence with three antibodies: two directed against the epitopes on the N terminus and C terminus of the heterologous fusion protein in the vector pRE4 and the third directed against region 2 of EBL-1. Both EBL-1 and the two regions of the pRE4 vector were expressed transiently on the surface of CHO-K1 cells. CHO-K1 cells expressing region 2 of EBL-1 bound to glycophorin B positive (+) erythrocytes, but not to glycophorin B-null erythrocytes of two unrelated donors, indicating that its erythrocyte receptor is glycophorin B (Fig. 5B). The binding of CHO-K1 cells expressing region 2 of EBL-1 to human erythrocytes was sensitive to neuraminidase and chymotrypsin treatment of the erythrocytes, but it was resistant to trypsin (Fig. 5B). The same

pattern of rosetting was observed when region 2 of EBL-1 was expressed on COS-7 cells. We found that the rosettes formed by region 2 of EBL-1 contained fewer erythrocytes than the rosettes formed by region 2 of EBA-175 (Fig. 5A). These rosettes were also less dense than those formed by region 2 of EBA-175 and region 2 of JESEBL/EBA-181. The region near the transmembrane sequence of EBL-1 did not bind human erythrocytes as would be expected. Region 2 of DBL-EBP in the *P. falciparum* genes is duplicated (F1 and F2 domains) compared with the *P. vivax* region 2 where only one copy is observed. The F1 and F2 domains of EBL-1 expressed alone on CHO-K1 cells did not bind to human erythrocytes, indicating that both domains are required for erythrocyte recognition.

Discussion

Here, we have provided evidence that the receptor for EBL-1, a member of the DBL-EBP family of receptors, is glycophorin B. First, EBL-1 from *P. falciparum* culture supernatant binds to glycophorin B⁺ and not to glycophorin B-null erythrocytes as indicated by immunoprecipitation with antibodies specific for region 2 of EBL-1. The immunoprecipitated protein was in the range of the predicted size of EBL-1. The antibodies specific for EBL-1 did not precipitate a protein from the supernatant of *P. falciparum* clone HB3 in which the *eb1-1* gene is deleted in the genome (9). Second, region 2 of EBL-1 expressed on the surface of CHO-K1 cells bound glycophorin B⁺ erythrocytes but not glycophorin B-null erythrocytes in two genetically unrelated glycophorin B-null individuals.

Glycophorin B has long been suspected to be a receptor for *P. falciparum* because of the high level of polymorphism in individuals living in malaria-endemic regions. However, because *P. falciparum* has multiple redundant pathways of invasion, no difference has been observed between the invasion of glycophorin B-null and glycophorin B-positive erythrocytes. For example, invasion of erythrocytes by the *P. falciparum* Dd2/Nm clone that expresses EBL-1 and the HB3 clone that lacks EBL-1 is similar compared with invasion of glycophorin B-positive erythrocytes (Dd2, 79%; HB3, 72%) (16).

EBL-1 and the other members of the DBL-EBP family share a high degree of sequence homology in region 2 and contain three exons at the 3' end that encode the transmembrane region and the cytoplasmic domain. EBL-1, however, differs in the 3' cysteine-rich region, the most conserved region of the DBL-EBP family, even between species, suggesting that EBL-1 has a unique function (1). The EBL-1 genes from ≈50% of *P. falciparum* clones have 5 thymidines inserted into the ORF that leads to a frameshift, suggesting that the gene is evolving to be a pseudogene.

Glycophorin B shows a high degree of polymorphism in malaria-endemic areas, including S-s-U-, Henshaw with variable sequence of the first 5 aa, and Miltenberger mutations that have recombination between glycophorin A and B (17). The Miltenberger mutations in malaria-endemic areas always lead to loss of glycophorin B. The most extreme example is the 59% gene frequency on S-s-U- erythrocytes in the Efe pygmies of the Ituri

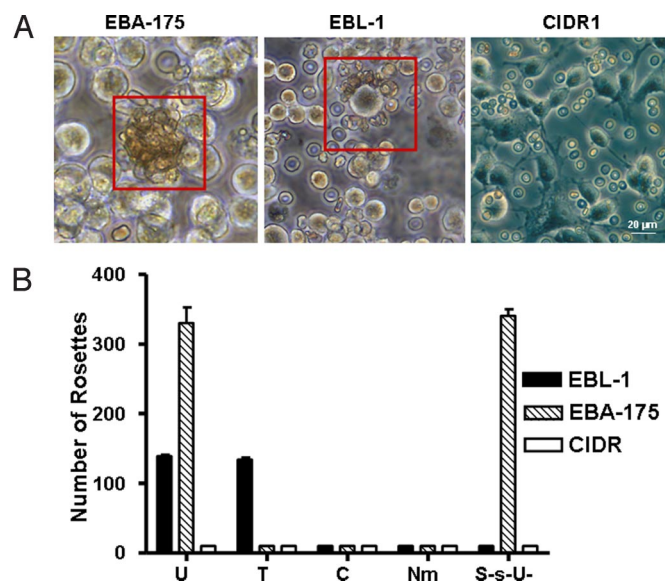


Fig. 5. EBL-1 expressed on CHO-K1 cells fails to bind to S-s-U- (glycophorin B-null) erythrocytes. (A) Region 2 is the erythrocyte-binding domain of EBL-1. Region 2 of EBL-1 was expressed on the surface of CHO-K1 cells. Transfected cells with five or more attached erythrocytes were counted, and the total per coverslip was recorded. The transfection efficiency of all constructs into CHO-K1 cells was 80–90%. Region 2 of EBA-175 and EBL-1 bound erythrocytes (red square), but not the control, CIDR1, the CD36-binding domain from PfEMP1. (B) Region 2 of EBL-1 has the same binding characteristics as the native protein in culture supernatant, binding to normal and trypsin-treated erythrocytes but not to S-s-U-, chymotrypsin-, or neuraminidase-treated erythrocytes. U, untreated erythrocytes; T, trypsin-treated erythrocytes; C, chymotrypsin-treated erythrocytes; NM, neuraminidase-treated erythrocytes; S-s-U-, glycophorin B-null erythrocytes. Approximately 130 rosettes were counted for each slide. Data are shown as the mean of three independent experiments, and the error bar denotes the SEM. (Scale bar, 20 μ m.)

DL6 and ID3 directed against the herpes simplex glycoprotein D sequences as described (11, 15, and gifts from R. Eisenberg and G. Cohen, University of Pennsylvania, Philadelphia), and rabbit polyclonal antisera directed against region II of EBL-1, respectively.

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